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FIG. 1A

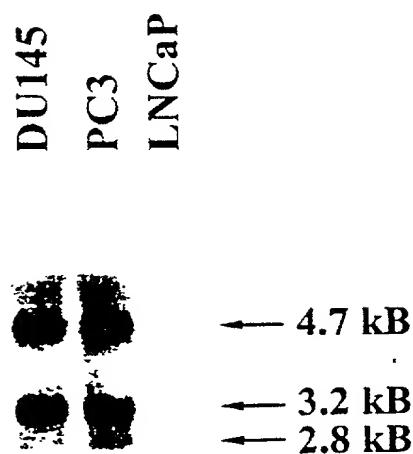


FIG. 1B

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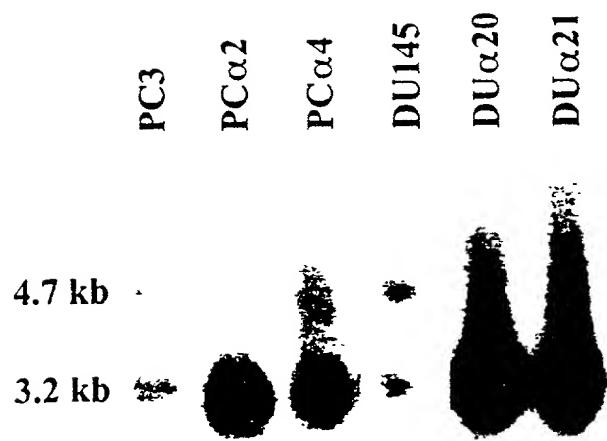


FIG.2

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DU145

DU $\alpha$ 20

DU $\alpha$ 21

FIG.3A

PC3

PC $\alpha$ 2

PC $\alpha$ 4

FIG.3B

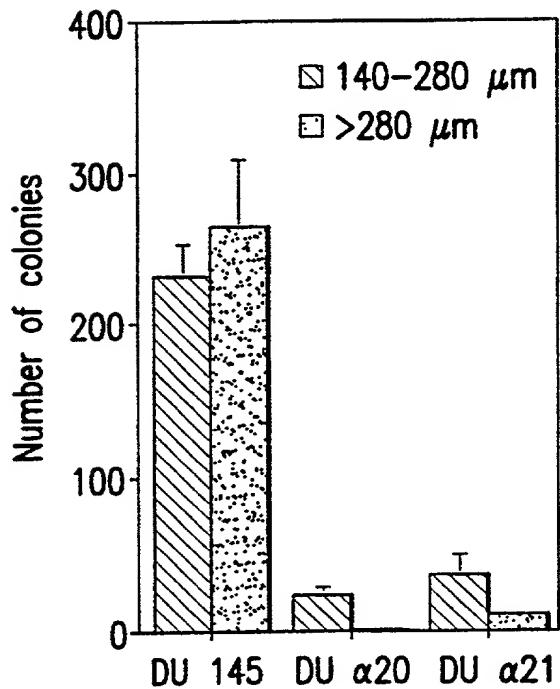


FIG.3A-1

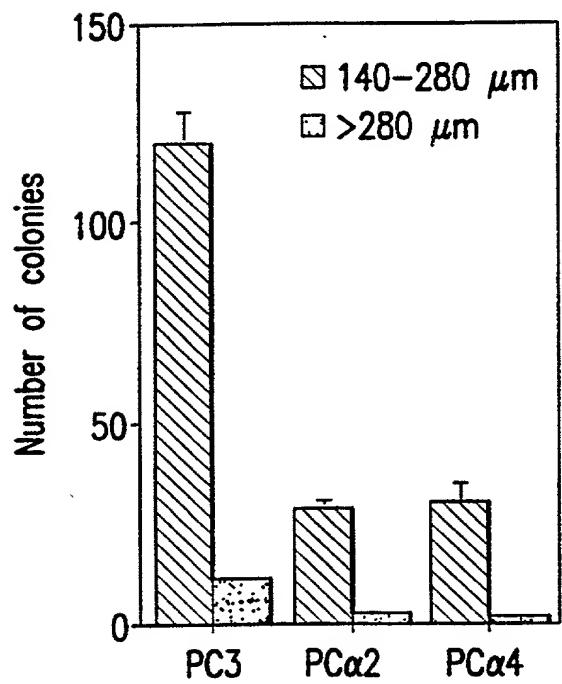


FIG.3B-1

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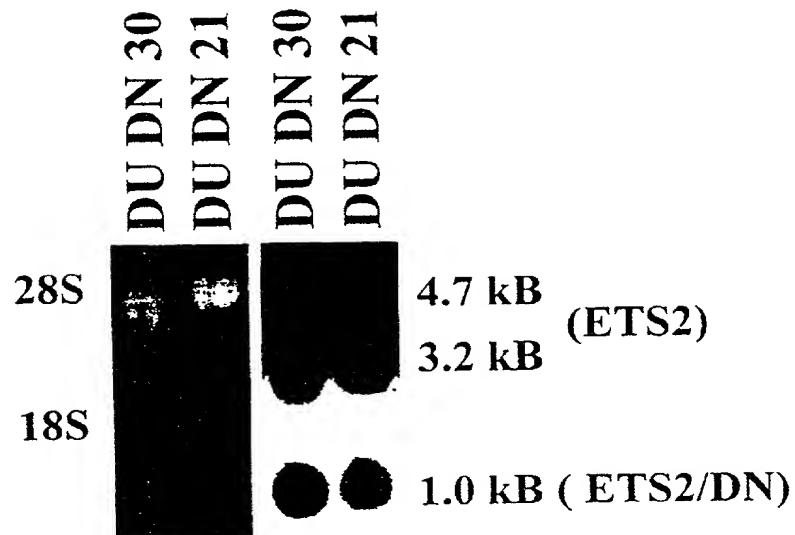


FIG.4A

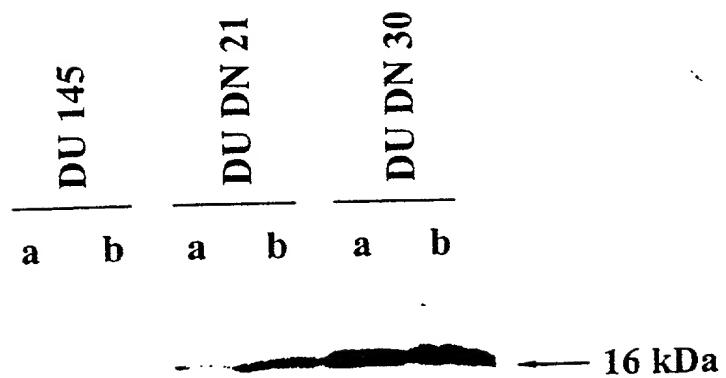


FIG.4B

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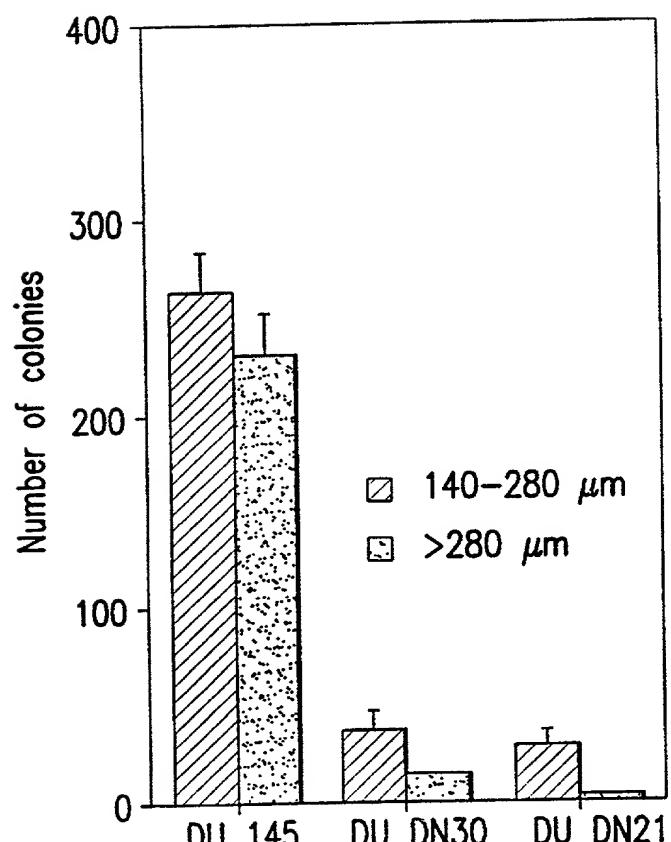


FIG.5

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CCGTTTCTC	CCCTCCCTC	CACTCGGCCG	TCCCTCCTTC	CTCCCTCCCTC	CTCCCTCCCTC	60
CTCCCGCTCC	TGAAGAGCGC	GCCGGCTGGG	GGACGGCCCG	GTACTTCCT	CCAGAGACTG	120
ACGAGTCCGG	TGTCGCTCCA	GCTCAGAGCT	CCCGGAGCGC	CCCGGCCAGC	GTCCGGCCTC	180
CCTGATCCTC	TCTGGCCGGC	GCCCTCGCCC	TCGCCCCGGG	CGCACCGAGC	AGCCGCGGGC	240
GCCCACCAAC	CACCGTCCCC	ACCAAGCGCC	GGCCCTGCC	GCAGGGCAG	GATGAATGAT	300
TTCGGAATCA	AGAATATGGA	CCAGGTAGCC	CCTGTGGCTA	ACAGTTACAG	AGGGACACTC	360
AAGGCCACGC	CAGCCTTGAT	CACCTTGAT	GGGTCCCTGT	TTGCTGTTT	TCCTTCTCTA	420
AATGAAGAGC	AAACACTGCA	AGAAGTGCCA	ACAGGCTTGG	ATTCCATTTC	TCATGACTCC	480
GCCAACGTG	AATTGCCCTT	GTTAACCCCG	TGCAGCAAGG	CTGTGATGAG	TCAAGCCTTA	540
AAAGCTACCT	TCAGTGGCTT	CAAAAAGGAA	CAGCGGGGCC	TGGGCATTCC	AAAGAACCCC	600
TGCGCTGGA	GTGAGCAACA	GGTATGCCAG	TGGCTCTCT	GGGCCACCAA	TGAGTTCACT	660
CTGGTGAACG	TGAATCTGCA	GAGGTTGGC	ATGAATGCC	AGATGCTGT	TAACCTTGGC	720
AAGGAACCGCT	TTCTGGAGCT	GGCACCTGAC	TTTGTGGCTG	ACATTCTCTG	CGAACATCTG	780
GACCAAATGA	TCAAAGAAAA	CCAAGAAAAG	ACAGAAGATC	AATATGAAGA	AAATTCAACAC	840
CTCACCTCCG	TTCCTCATTC	GATTAACAGC	AATACATTAG	GTTTGGCAC	AGAGCAGGCG	900
CCCTATGGAA	TGCAGACACA	GAATTACCCC	AAAGGCGGCC	TCCTGGACAG	CATGTGTCCG	960
GCCTCCACAC	CCAGCGTACT	CAGCTCTGAG	CAGGAGTTTC	AGATGTTCCC	CAAGTCTCGG	1020
CTCAGCTCCG	TCAGCGTCAC	CTACTGCTCT	GTCAGTCAGG	ACTTCCCAGG	CAGCAACTTG	1080
AATTGCTCA	CCAACAAATTC	TGGGACTCCC	AAAGACCACG	ACTCCCCTGA	GAACGGTGGC	1140
GACAGCTTCG	AGAGCTCAGA	CTCCCTCCTC	CAGTCTGGA	ACAGCCAGTC	GTCCCTGCTG	1200
GATGTGCAAC	GGGTTCCCTC	CTTCGAGAGC	TTCGAAGATG	ACTGCAGCCA	GTCTCTCTGC	1260
CTCAATAAGC	CAACCATGTC	TTTCAAGGAT	TACATCCAAG	AGAGGAGTGA	CCCACTGGAG	1320
CAAGGCAAAC	CAGTTATACC	TGCAGCTGTG	CTGGCCGGCT	TCACAGGAAG	TGGACCTATT	1380
CAGCTGTGGC	AGTTTCTCCT	GGAGCTGCTA	TCAGACAAAT	CCTGCCAGTC	ATTCATCAGC	1440
TGGACTGGAG	ACGGATGGGA	TTTAAGCTC	GCCCACCCCC	ATGAGGTGGC	CCGCCGGTGG	1500
GGAAAGAGGA	AAAATAAGCC	CAAGATGAAC	TACGAGAAGC	TGAGCCGGGG	CTTACGCTAC	1560
TATTACGACA	AGAACATCAT	CCACAAGACG	TCGGGAAAGC	GCTACCTGTA	CCGCTTCGTG	1620
TCCGACCTCC	AGAACTTGCT	GGGGTTCACTC	CCCGAGGAAC	TGCACGCCAT	CCTGGGGCGTC	1680
CAGCCCCGACA	CGGAGGACTG	AGGTGCGCCG	GACCACCTG	AGCCGGCCCC	AGGCTCGTGG	1740
ACTGAGTGGG	AAGCCCACATCC	TGACCAAGCTG	CCTCCGAGGA	CCCAGGAAAG	GCAGGATTGA	1800
AAATGTCCAG	GAAAGTGGCC	AAGAAGCACT	GGCCTTATTG	CATCCCAAAC	CACGCCTCTT	1860
GACCAGGCTG	CCTCCCTTGT	GGCAGCAACG	GCACAGCTAA	TTCTACTCAC	AGTGCTTTA	1920
AGTGAAAATG	GTCGAGAAAG	AGCCACCGGG	AAGCCGTCT	GGCGCTGGC	AGTCCGTGGG	1980
ACGGGATGGT	TCTGGCTGTT	TGAGATTCTC	AAAGGAGCGA	GCATGTCGTG	GACACACACAA	2040
GACTATTTT	AGATTTCTT	TTGCCCTTTG	CAACCAGGAA	CAGCAAATGC	AAAAACTCTT	2100
TGAGAGGGTA	GGAGGGTGGG	AAGGAAACAA	CCATGTCATT	TCAGAAGTTA	GTGCTATAT	2160
ATTATAATAA	TCTTATAAATT	GTTCAGAA	TCCCTTAACA	GTGCTATTA	ACAGAAATTG	2220
TATATTGTAA	TTTAAATAA	TTATATAACT	GTATTTGAAA	TAAGAATT		2269

FIG.6

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Met Asn Asp Phe Gly Ile Lys Asn Met Asp Gln Val Ala Pro Val Ala  
1 5 10 15  
Asn Ser Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe  
20 25 30  
Asp Gly Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr  
35 40 45  
Leu Gln Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala  
50 55 60  
Asn Cys Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser  
65 70 75 80  
Gln Ala Leu Lys Ala Thr Phe Ser Gly Phe Lys Lys Glu Gln Arg Arg  
85 90 95  
Leu Gly Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys  
100 105 110  
Gln Trp Leu Leu Trp Ala Thr Asn Glu Phe Ser Leu Val Asn Val Asn  
115 120 125  
Leu Gln Arg Phe Gly Met Asn Gly Gln Met Leu Cys Asn Leu Gly Lys  
130 135 140  
Glu Arg Phe Leu Glu Leu Ala Pro Asp Phe Val Gly Asp Ile Leu Trp  
145 150 155 160  
Glu His Leu Glu Gln Met Ile Lys Glu Asn Gln Glu Lys Thr Glu Asp  
165 170 175  
Gln Tyr Glu Glu Asn Ser His Leu Thr Ser Val Pro His Trp Ile Asn  
180 185 190  
Ser Asn Thr Leu Gly Phe Gly Thr Glu Gln Ala Pro Tyr Gly Met Gln  
195 200 205  
Thr Gln Asn Tyr Pro Lys Gly Gly Leu Leu Asp Ser Met Cys Pro Ala  
210 215 220  
Ser Thr Pro Ser Val Leu Ser Ser Glu Gln Glu Phe Gln Met Phe Pro  
225 230 235 240  
Lys Ser Arg Leu Ser Ser Val Ser Val Thr Tyr Cys Ser Val Ser Gln  
245 250 255  
Asp Phe Pro Gly Ser Asn Leu Asn Leu Leu Thr Asn Asn Ser Gly Thr  
260 265 270  
Pro Lys Asp His Asp Ser Pro Glu Asn Gly Ala Asp Ser Phe Glu Ser  
275 280 285  
Ser Asp Ser Leu Leu Gln Ser Trp Asn Ser Gln Ser Ser Leu Leu Asp  
290 295 300  
Val Gln Arg Val Pro Ser Phe Glu Ser Phe Glu Asp Asp Cys Ser Gln  
305 310 315 320  
Ser Leu Cys Leu Asn Lys Pro Thr Met Ser Phe Lys Asp Tyr Ile Gln  
325 330 335

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Glu Arg Ser Asp Pro Val Glu Gln Gly Lys Pro Val Ile Pro Ala Ala  
340 345 350  
Val Leu Ala Gly Phe Thr Gly Ser Gly Pro Ile Gln Leu Trp Gln Phe  
355 360 365  
Leu Leu Glu Leu Leu Ser Asp Lys Ser Cys Gln Ser Phe Ile Ser Trp  
370 375 380  
Thr Gly Asp Gly Trp Glu Phe Lys Lau Ala Asp Pro Asp Glu Val Ala  
385 390 395 400  
Arg Arg Trp Gly Lys Arg Lys Asn Lys Pro Lys Met Asn Tyr Glu Lys  
405 410 415  
Leu Ser Arg Gly Leu Arg Tyr Tyr Asp Lys Asn Ile Ile His Lys  
420 425 430  
Thr Ser Gly Lys Arg Tyr Val Tyr Arg Phe Val Cys Asp Leu Gln Asn  
435 440 445  
Leu Leu Gly Phe Thr Pro Glu Glu Leu His Ala Ile Leu Gly Val Gln  
450 455 460  
Pro Asp Thr Glu Asp  
465

FIG.7B

SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-	SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-
ETS1 HUMAN	ETS1 MOUSE
SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-	SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-
ETSB CHICK	ETSA XENLA
SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-	SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-
vETS E26	ETS2 XENLA
SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-	SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-
ETS2 HUMAN	ETS2 MOUSE
SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-	SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-
ETS2 CHICK	ETS2 SEAUR
SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-	SG-P1QLWQFLLELLTDKS-COSF1SWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKLSRGLRYYDKNIIRKTA-GKRYVYRFV-
DROME	FL11 MOUSE
SG-Q1QLWQFLLELLSDSA-NASC1TWEGL-TNGEFKMT--DPDEVARRWGKRK-SKPMMNYDQLSRALRYYDKNIMTKVH-GKRYAYKFD-	SG-Q1QLWQFLLELLSDSS-NASC1TWEGL-TNGEFKMT--DPDEVARRWGKRK-SKPMMNYDQLSRALRYYDKNIMTKVH-GKRYAYKFD-
ERG HUMAN	ETS3 DROME
GSGQ1Q WQPLLELSDSN-NASAISWEG-QSGEFLR1--DPDEVARRWGKRK-AKPMMNYDQLSRALRYYDKNIMTEVH-GKRYAYKFD-	GSGQ1Q WQPLLELSDSN-NASAISWEG-QSGEFLR1--DPDEVARRWGKRK-AKPMMNYDQLSRALRYYDKNIMTEVH-GKRYAYKFD-
GABP RAT	ETS6 DROME
SGGQ1QLWQPLLELLADSS-NANAISWEG-DEGEFLN--QPELVAQKWCQRK-NKPTMNYPKLSRALRYYDKDM1CKVQ-GKGFVYKFV-	SGGQ1QLWQPLLELLADSS-NANAISWEG-DEGEFLN--QPELVAQKWCQRK-NKPTMNYPKLSRALRYYDKDM1SKVS-GQKFVYKFV-
DELG DROME	PEA3 MOUSE
NG-Q1QLWQFLLELLTDKD-ARDC1SWVG-DEGEFLN--QPELVAQKWCQRK-NKPTMNYPKLSRALRYYDKDM1CKVQ-GKGFVYKFV-	NG-QVQLWQFLLE1TDCE-HTDVIEWG-TEGEFL1--DPDRVARIWGEKK-NKPTMNYPKLSRSLRYYYEKG1MQKVAGERRYVYKFV-
ELK HUMAN	SAP1 HUMAN
MDPSVTLWQFLLQLREQG-NCHTSNTSRDGGEFLKV--DAEEVARLGCRK-NKPAWMNYDQLSRALRYYDKN1IRKVS-GQKFVYKFV-	MDSAITLWQFLLQLQKPP-NKHMICWTSDG-QFL1--QAEVARLGIRK-NKPAWMNYDQLSRALRYYDKN1IRKVS-GQKFVYKFV-
ELKK MOUSE	
ELF1 HUMAN	
E74A DROME	
EGSTTYLWEFLKLQLDREYCPRF1KWTREKGIPK1--DSRVAKLWGRRK-NRPMNYDQLLRS1RQYYKKG1MKKSERSQRVYQFC	GGSHIHLWOFLKELLASPVQNGT1RW1DRSKGIPK1--DSRVAKLWGRRK-NRPMNYDQLLRS1RQYYKKG1MKKSERSQRVYQFC
ETS4 DROME	PUI MOUSE
SKKKIRLYQFLLDLRLSGDM-KDSTIWWVDKDGTQFSSKHEALAHRC1QKGNRKKNTYQKMARALRN1GKTEVKVK--KLTYQF-S	SKKKIRLYQFLLDLRLSGDM-KDSTIWWVDKDGTQFSSKHEALAHRC1QKGNRKKNTYQKMARALRN1GKTEVKVK--KLTYQF-S
PUI HUMAN	

FIG. 8A

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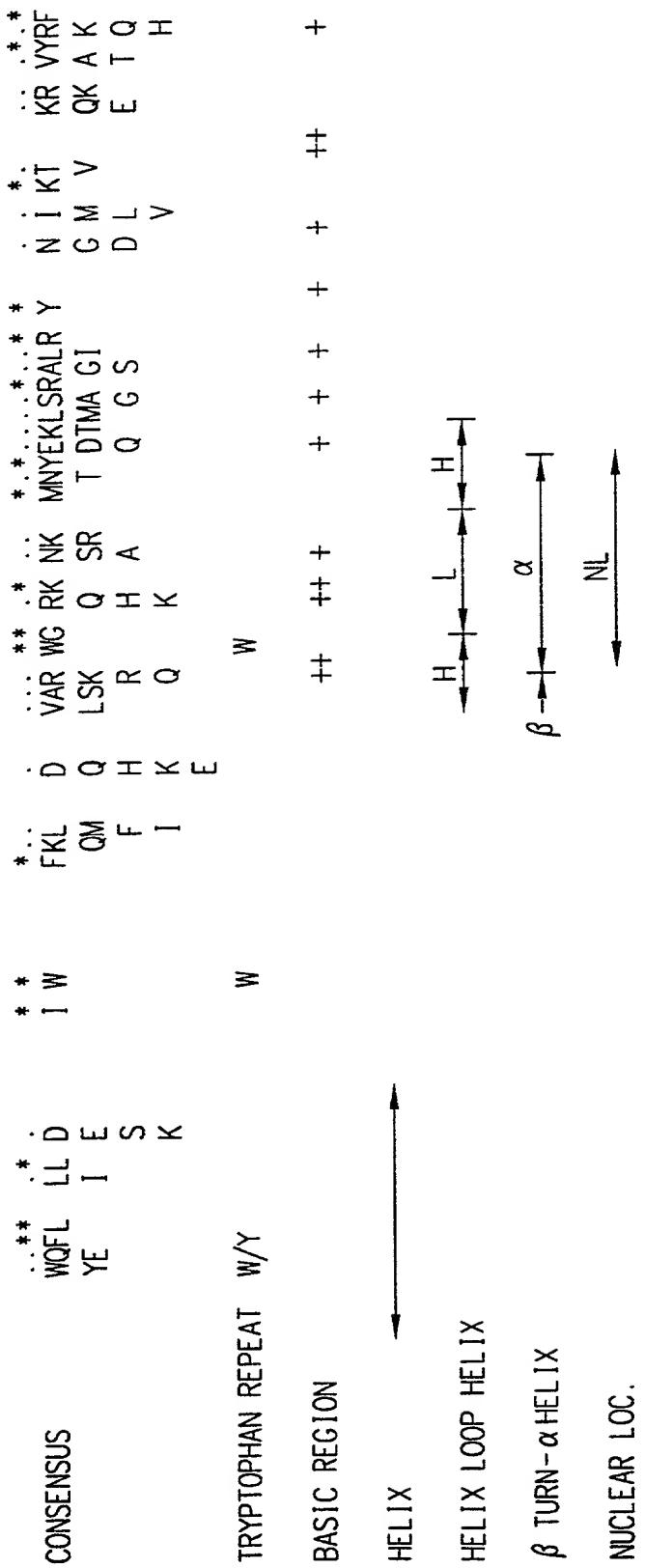


FIG. 8B

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ETS2 IN 289

289  
289 T  
289 D

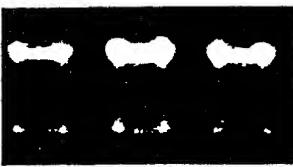


FIG.9A

ETS1 IN 289

289  
289 T  
289 D



FIG.9B

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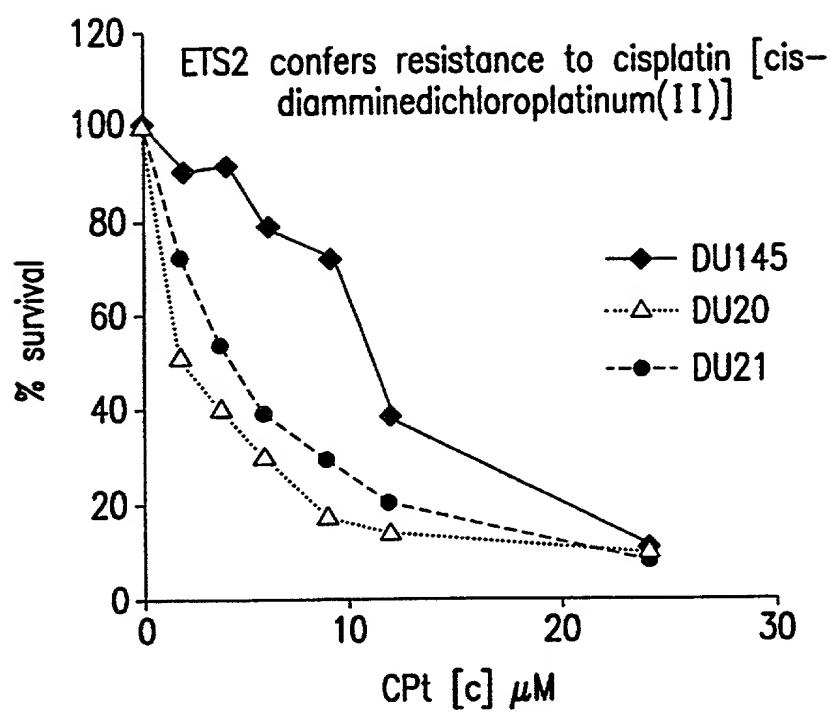


FIG. 10